

Figure 1

ERRL1	MAGNDCCGALLDEELSSFFLNLYLSDTQGGDSGEEQ-LCADLPELDLSQLDASDFDSATCLG	59
PGC-1	MAWDMCSQDSVWSIDIECAALVGEDQPLCPDLPELDLSELDVNDLDTDSFLG	51

ERRL1	ELQWCPETSETEPSQYSPDDSELFQ-IDSENEA-LLAALTKTLDIPEDDVGLAAPPELD	117
PGC-1	GLKWCSQSEIISNQYNNEPANIFEKIDEENEANLLAVLTETLDSLFVDEGLPSTFDALT	111

ERRL1	EGDTPSCTPASAPPLSAPPSPTLERLLSPASDVDELSSLQKLLLATSSPTASSDALKDGA	177
PGC-1	DGAVTTDNEASPSSM---PDGT-----PPQEAEEFSLKKLLAPANTQLSYNECSGLS	163

ERRL1	TWSQTSLSS---RSQRPCVKVDGTQDKKPTL---RAQSRPCTELHKHLTSVLPCPRVK	230
PGC-1	TQNHAANHTRIRTNPAIVKTENSWSNKAKSICQQQKPPRRPCSELLKYLTNDPPHTK	223

ERRL1	ACSPTPHFSPRLLSKEE-----EEVGEDCPSPW--LTPASQDLSAQDTASPDQAQPF	282
PGC-1	PTENRNSSRDKCAKSKSHTQPSQHAQAKPTTSLPLTPESPNDP---KGSFFEN---	276

ERRL1	EEDVRAMVQLIRYMHTYCLPQRKLPQRAPEPIFOACSSLSRQVQPRSRHPKAFWTEFSI	341
PGC-1	-----	
ERRL1	LRELLAQDILCDVSKPYRLAIPVYASLTPQSRPRPFKDSQASPAHSAMAEVRITASPKS	401
PGC-1	-----	
ERRL1	TGPRPSLRPLRLLEVKRDNKPTRQKREDEEEEEEEEEEEEEKEEEEEEWGRKRPGRGLP	461
PGC-1	-----	
ERRL1	WTKLGRKMDSSVCPVRRSRRLNPELGPWLTTDEPLGALPSMCLDTETHNLEEDLGSITD	521
PGC-1	-----	
ERRL1	SSQGRQLPQGSQIPALESFCESGCGDTDEDPCFPQPTSRDSSRCLMLALSQSDSLGKXSF	581
PGC-1	-----KTI	279

ERRL1	BESLTVELCGTAGLTPPTTPPYKMEEDPFKPDTKLSPGQDTAPSLPSPEAL--PLTATP	639
PGC-1	ERTLSVELSGTAGLTPPTTPPHKANQDNPFKASPKLPCKTVVPPTKRARYSECSGTQ	339

ERRL1	GASHKLKPNHPPERSEILSHLQHAT--TQVVSQAGQKRPFCSCSFGDHDYQVLRPEAALQR	697
PGC-1	G-SHST-KKGPEQSEIYAQLSKSSGLSRGHEERKTKRPSLRLFGDHDYQVLSNKTDLI	397

ERRL1	KV---LRSWEPGVHLEDLAQQGAPLPTETKAP---RR--EANQNCDPHKDSMQLRDHE	749
PGC-1	NISQELQDSRQLDFKDASCDWQHICSSDTSQCYLRETLEASKQVSPCSTRK-QLQDQE	456

ERRL1	IRASLTKHFGLETALEGEDLASCKSPEDYTVFEDSSSS-----SGES-SFLEEEEE	802
PGC-1	IRAEINXKHFGHPCQAVF-DDKSDKTSELRDGDFSNEQFSKLPVFINSGLAMDGLFDDSED	515

ERRL1	EEEGGEEDDEGEDS---GVSPFCSD-HCFYQ---SPP---SKASRQLCSFRRSSSGSS	851
PGC-1	ESDKLSYPWDGTQPYSLFDVSPSCSSFNSPCRDSVSPPKSLFSQRPORMSRSRSESRNB	575

ERRL1	SCS-----SWSPATRIQ-----FRRESRGPCS-----DG	875
PGC-1	SCSRSPYRSRGRSPGSRSSSRSCYVYESSHYRHRTNRNSPLYVRSRSPYRRPYDS	635

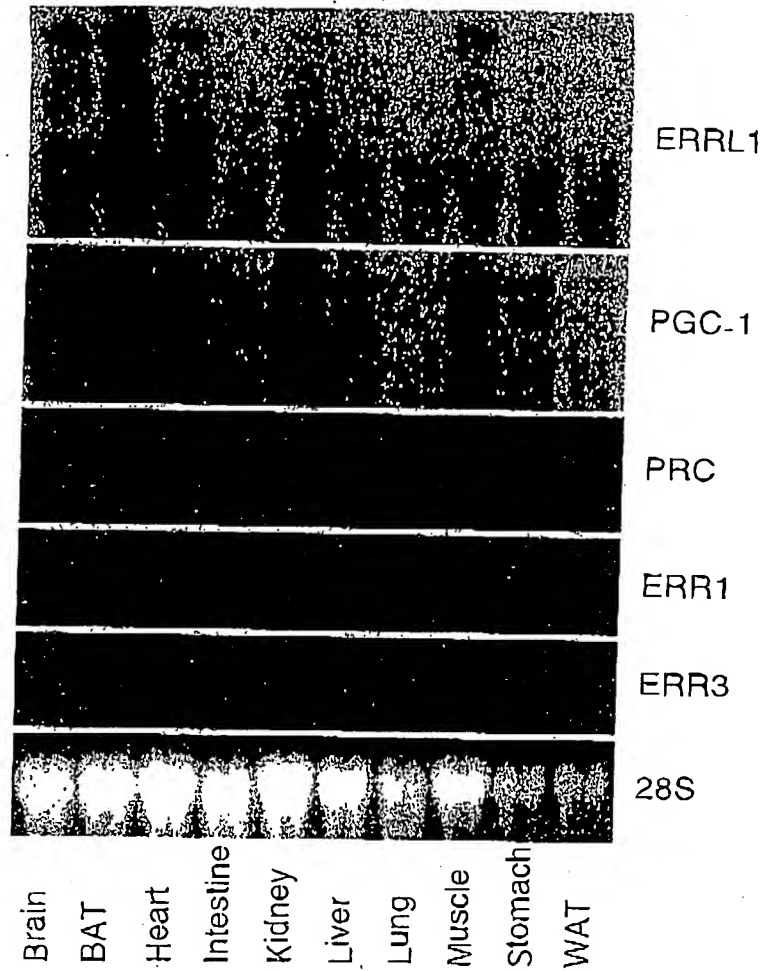
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PGC-1	YEAYEHERLKRDEYRKEHEKRESERAKORERQKQKAIERHVIYVGKIRPDTTRTELDR	695

ERRL1	FEVFGIEVCQVLTIRSKRGQKHGFIITFR--CSEHAALSVRNGATLKRNEPSFHLISYGG	971
PGC-1	FEVFGIEIECTVNIIRDD-GDSYGFITYRYTCDAFAL--ENGYTLRSNETDFELYFCGR	752

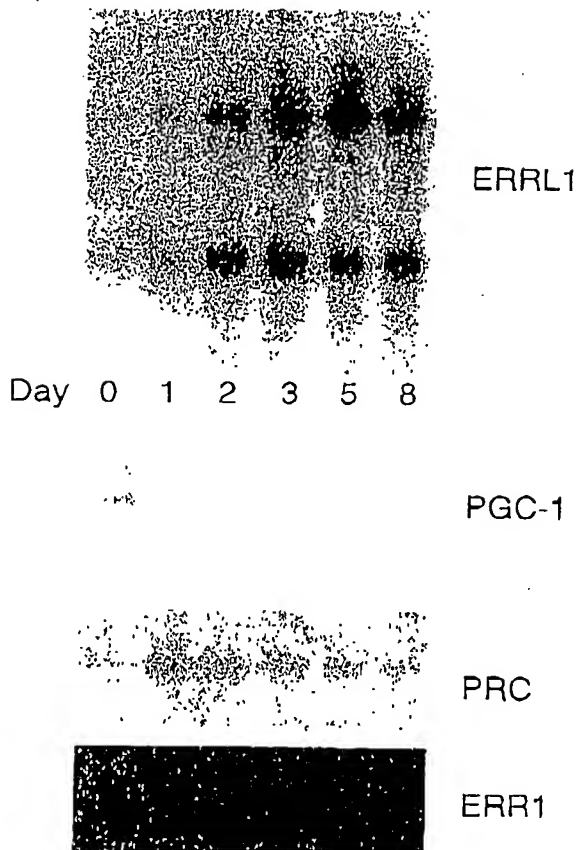
ERRL1	RHFRWPRYTDYDPTSEESLPSSGKSKYEAMDFDSLLKEAQQLH	1014
PGC-1	KQFFKSNYADLDTNSDDFDPASTKSKYDSLDFDSLLKEAQRSLR	796

Figure 2

a



b



c

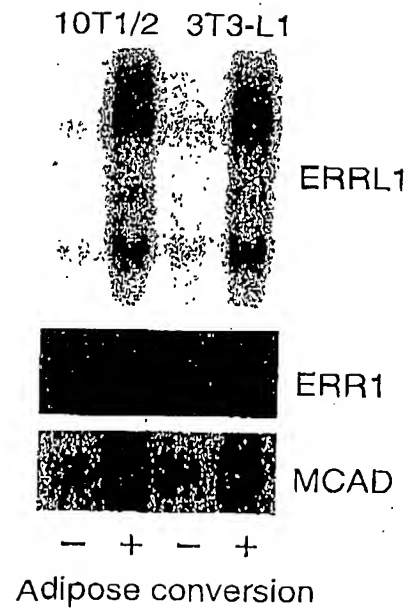


Figure 3

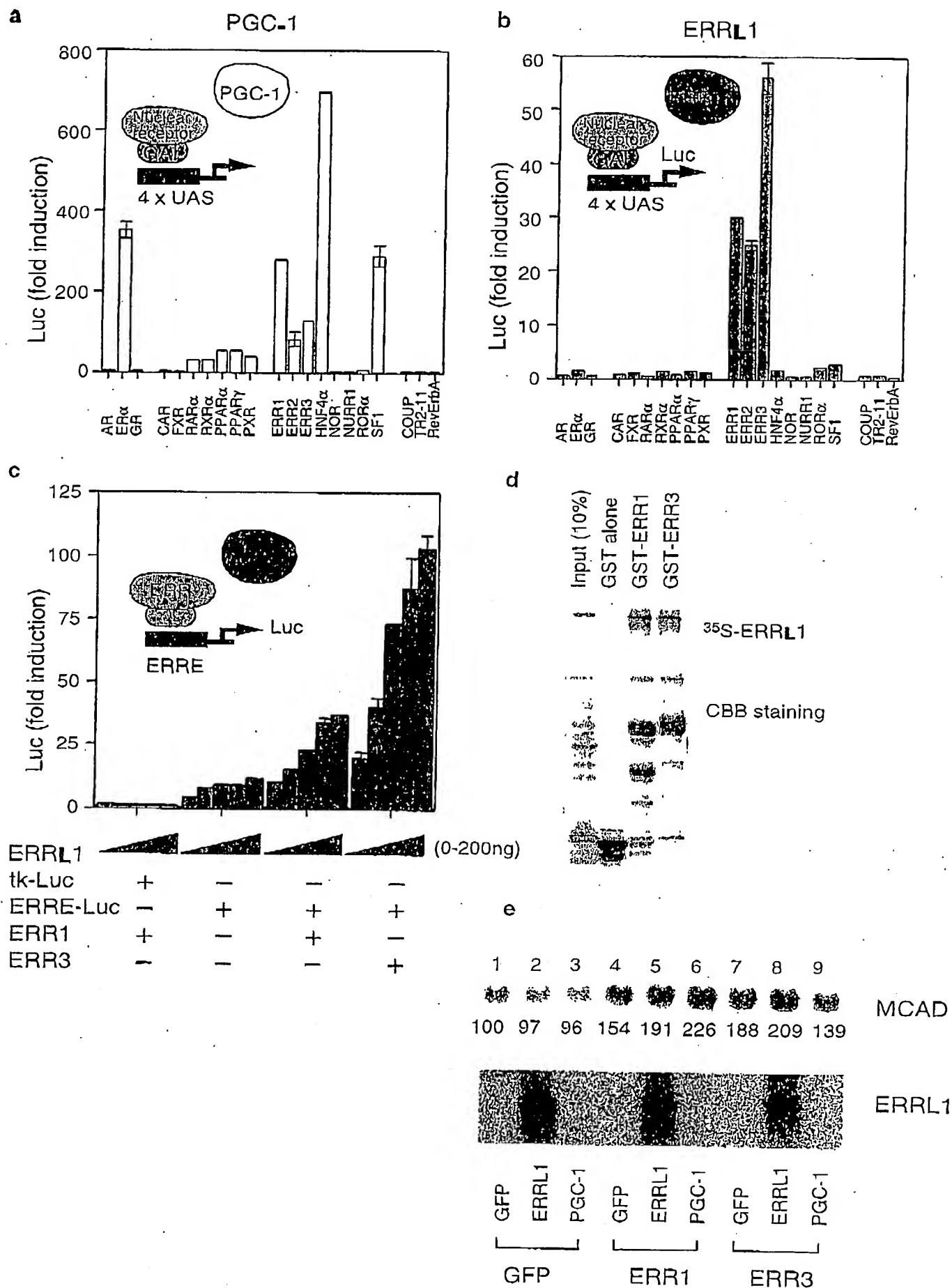


Figure 4

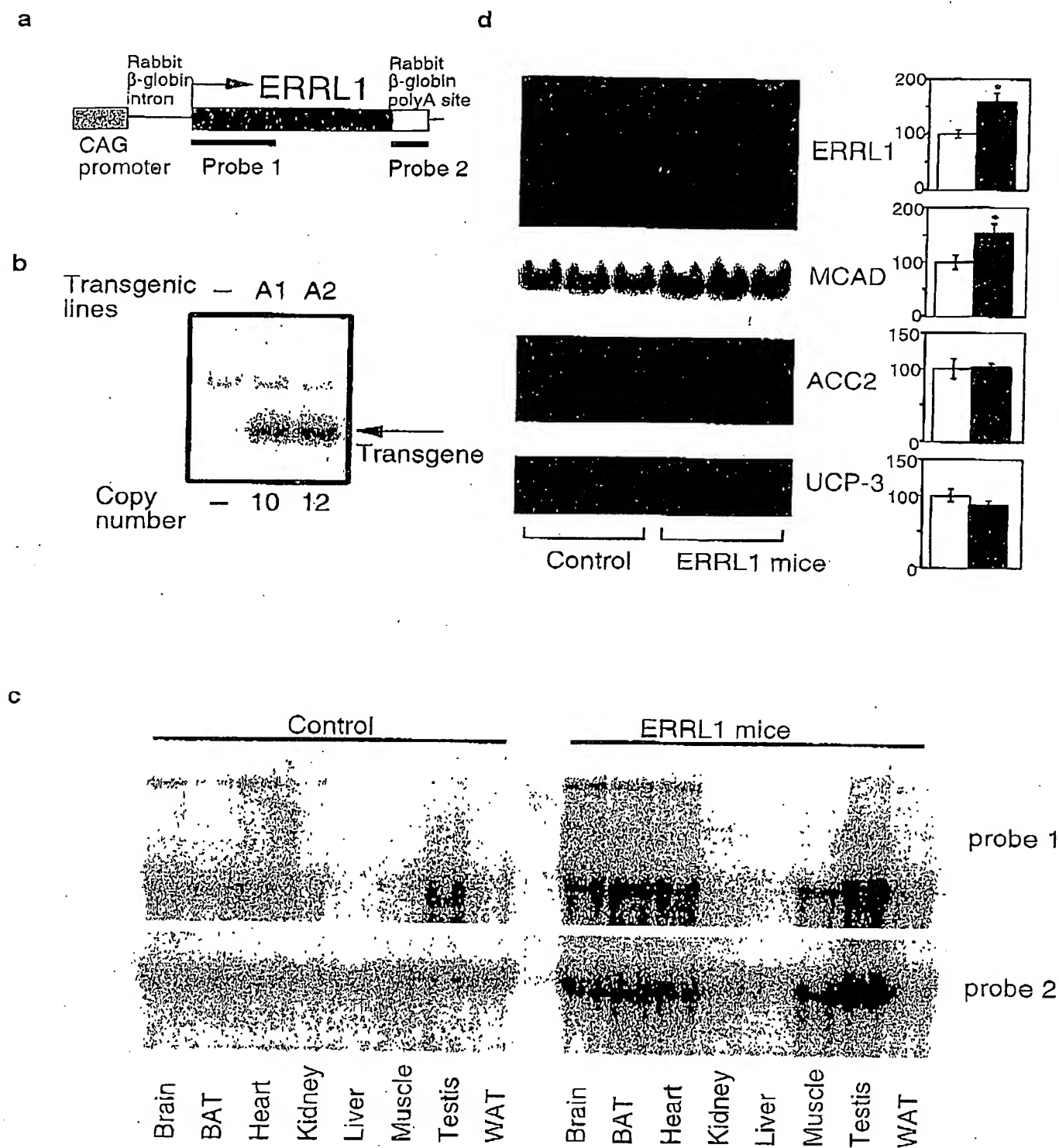


Figure 5

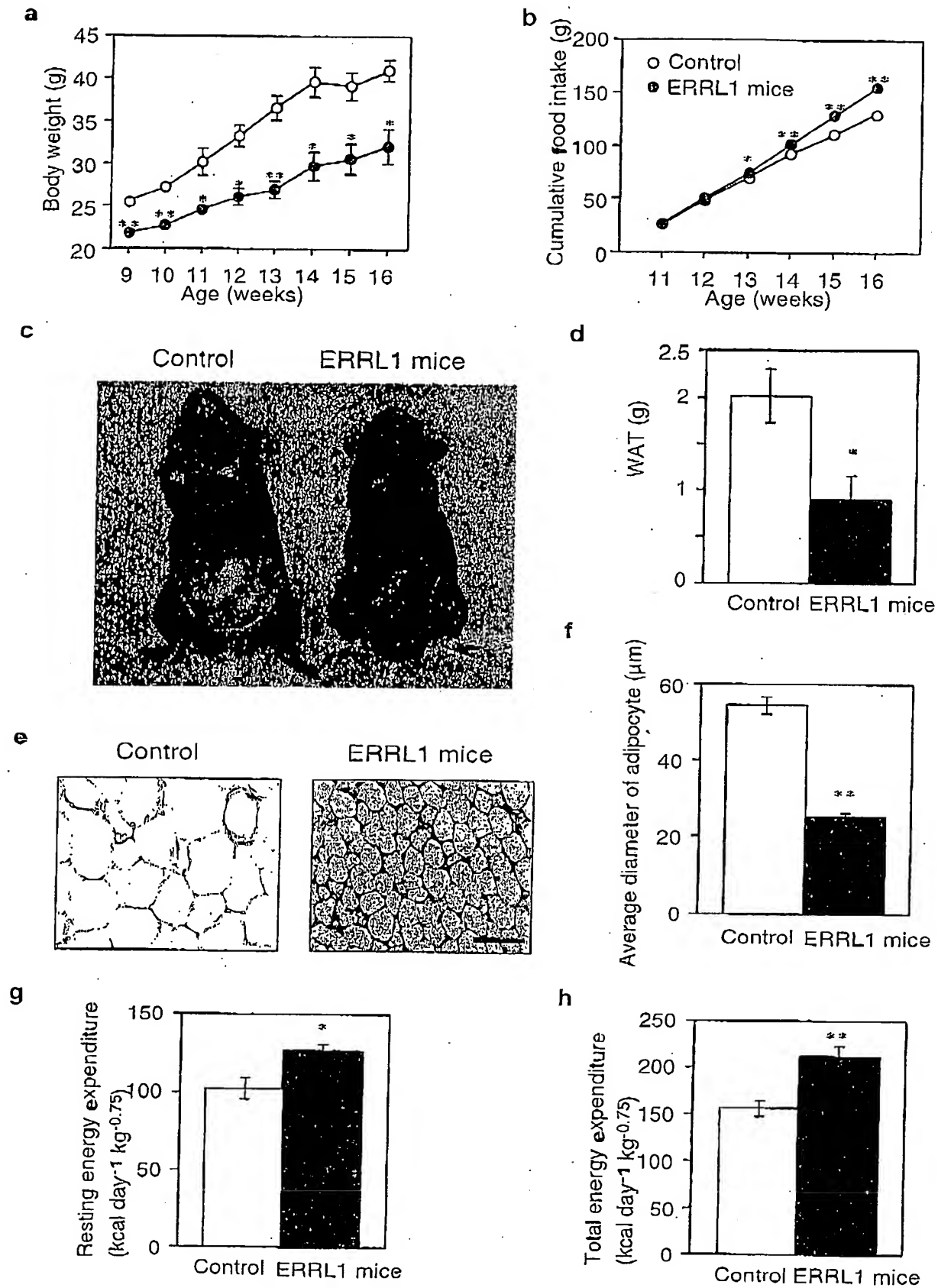


Figure 6

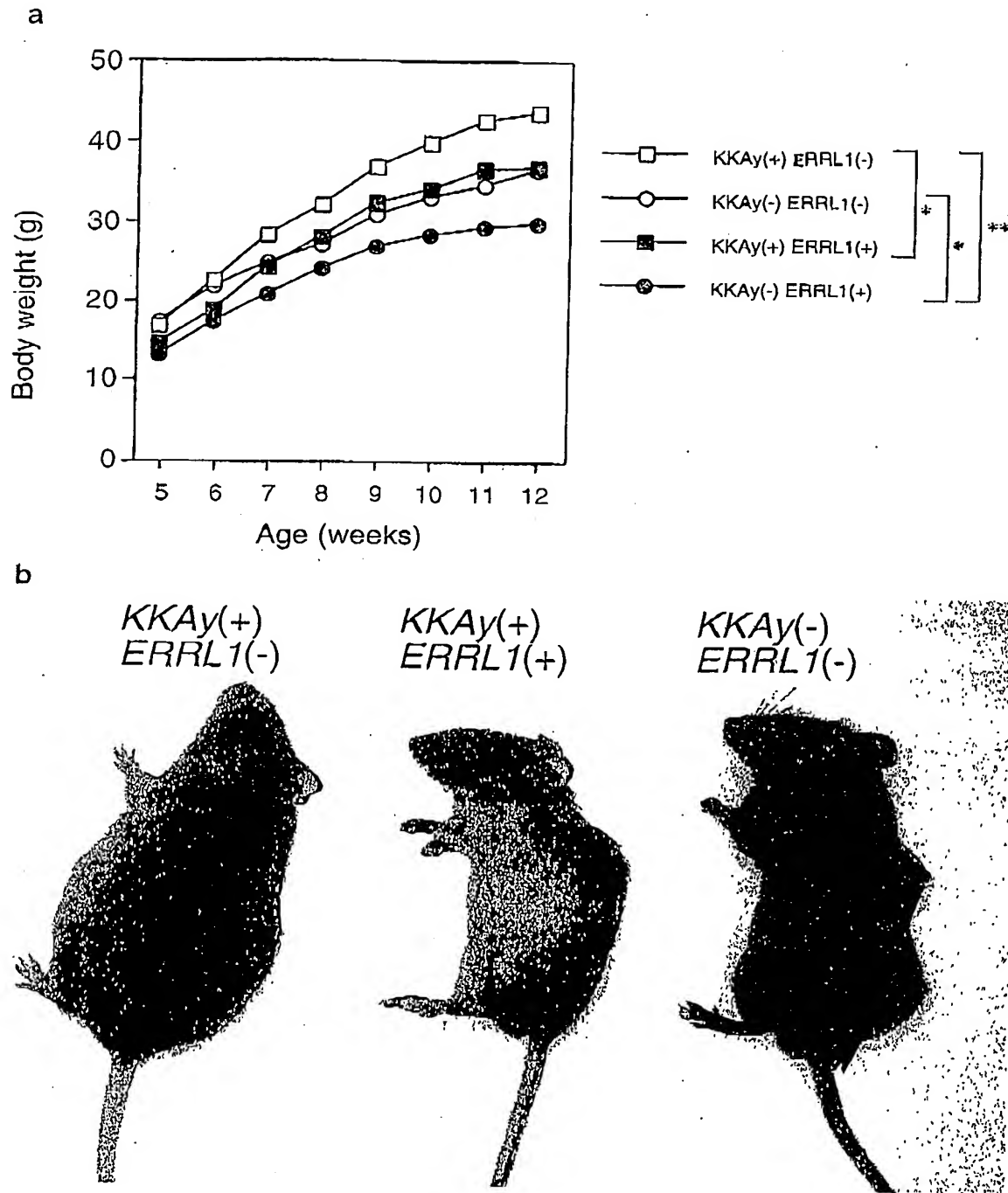
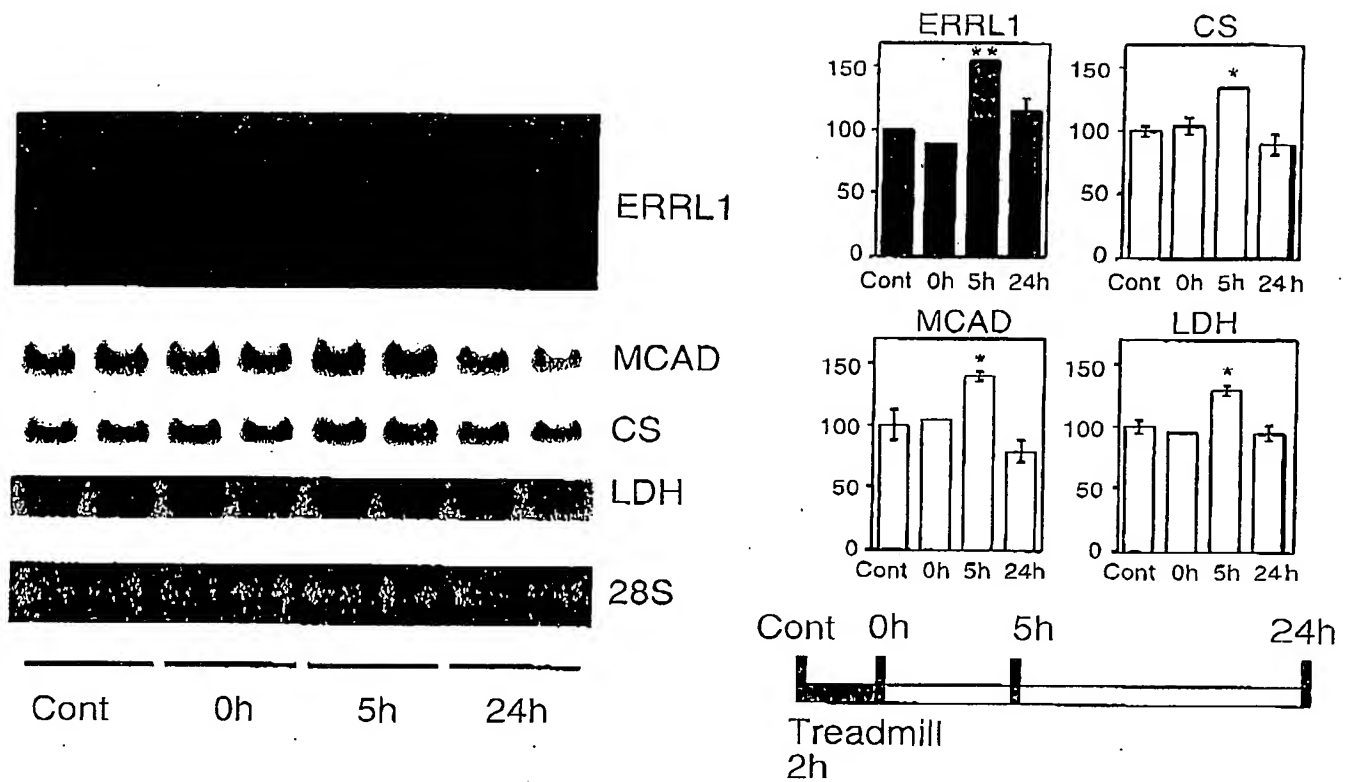


Figure 7

a



b

